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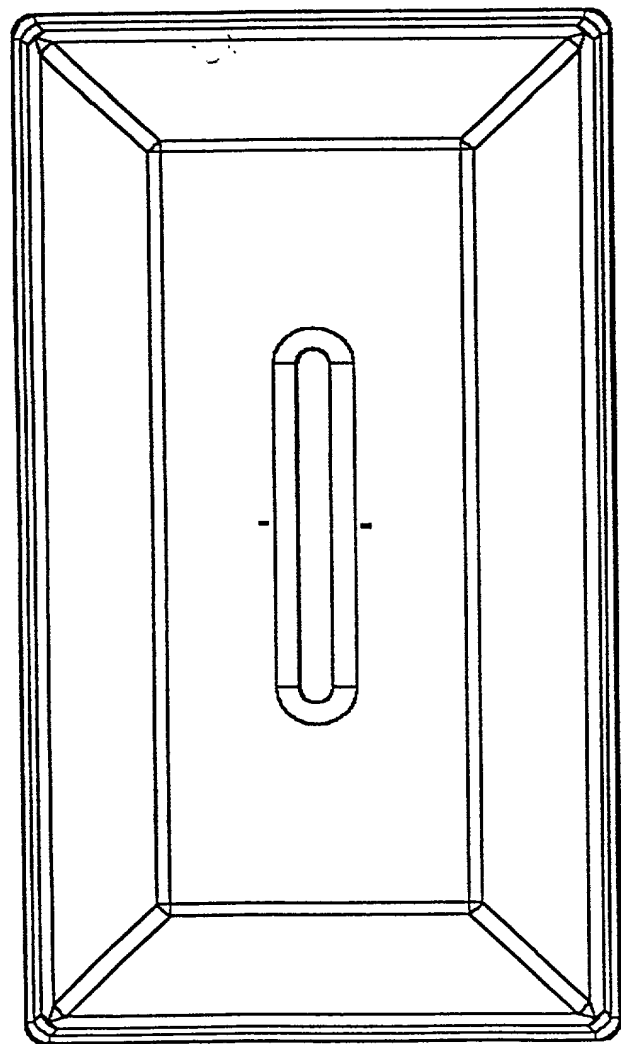


Figure 1A

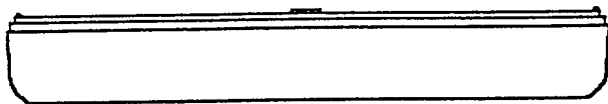


Figure 1C

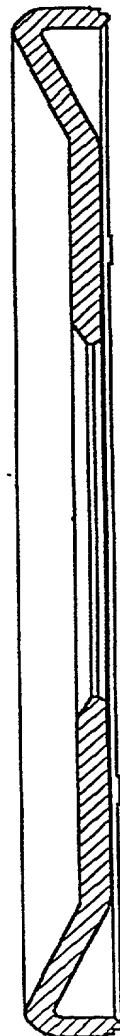


Figure 1B

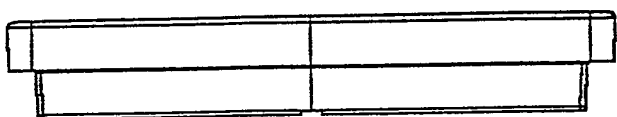


Figure 2C

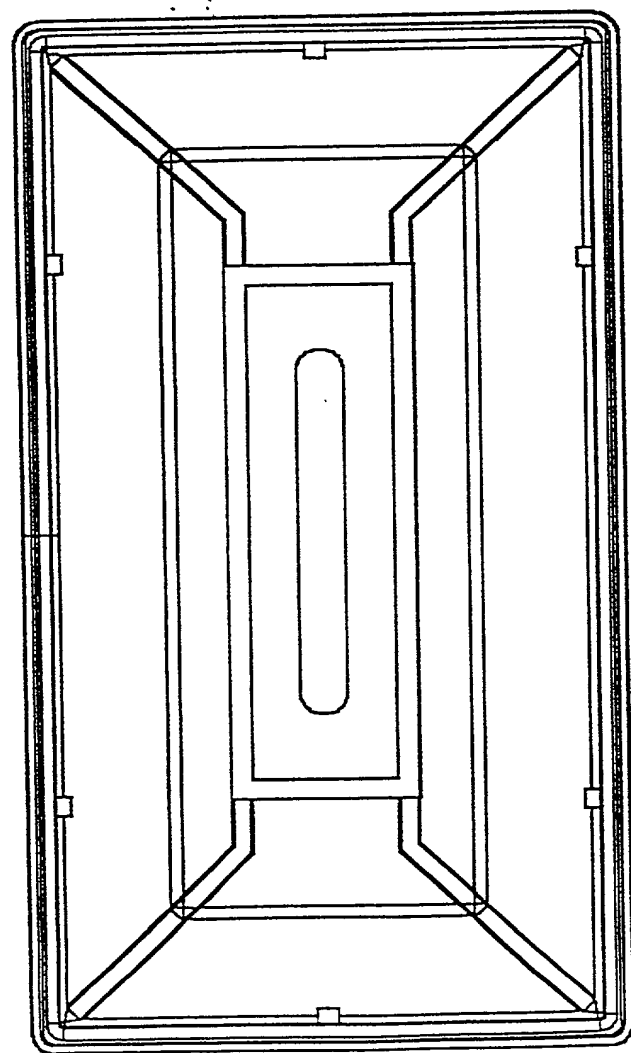


Figure 2A

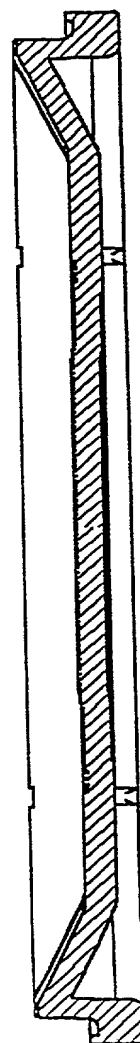


Figure 2B

Figure 3A

Nucleotide sequence of *Cryptosporidium parvum* protein disulfide isomerase cDNA

5 001 atgacgga ttagagctt ggtttcagca gcatttttag gtttttcttg tcttccaag
061 gtagtcttg gtggagatga agtcaactc atttcagaac acattacttc cttaacttcc
121 tccaacttcg aagacttcat taagagcaag gaacacgtaa ttgttacttt ctttgcccc
181 tggcgccggtc attgtactgc tttagagcca gaattcaagg caacatggcg tgaatctca
241 aagctctctc cccagtaga ctgtggcagt gttgatgcaa ctgaaaatat ggagcttgca
10 301 caacaatatg gtgtgagcg ataccaccc atcaattctc tcagtggatc tgacagtgtt
361 cagaactatt caggagcaag aagcaaggat gcattcatca agtatattaa gaagttgacc
421 ggaccagcag tccaagtgc tgaatcagaa gaagctatca agacaattct cgcttcttct
481 tcttcagcct ttgttgaag attcacctct aaggactcag ctgagtatgc tgtcttcgag
15 541 aaggttgcta gtggtcaccg cgagcacaac tatgctttca ttgcttcttc ccaagaagg
601 gaacaaaagc tcgaggtatt acacaaggac gaggagccag ttctctctcc aatgccaaag
661 actgttgaag agttggagg caagatatcc ataatgaatg taccattgtt ctctgcaatt
721 agtgctgaga actactcct ctatatgtca agagaagggt atactgcctgg ttctgtggt
782 ctaacgagga cttcgccaag tatgcttcaa acattagaaa ggttcagct gattacagag
20 842 aaaagtatgc cttgttttc _cttgatact gagcaatttg gttcccatgc tactcaacat
901 ctcttaattg agaaattccc aggtttggtt atccaaagtg tcaatgttcc atcaattaga
961 tacatgtatg gtccagctaa attcgactct gttgagccat taaaggaatt tatgaagcaa
1021 gtttctgaag gcaagcacga actcagcatt aagtctgagc caatccagc tgagcaatct
1081 ggtccagtca ctgttggtgt tggtaagacc ttcgaagaaa ttgttttcag aagtgacaag
25 1141 gatgttcttt tggaaatcta tgcccaatgg tgtggacact gtaagaacct cgagccaatc
1201 tacaaccaac tcggcgaaga gtacaaggac aacgacaagg ttgtgattgc aaagatcaat
1261 ggaccacaaa acgatatccc atatgaagg ttccagtcca gagccttccc aactatcttg
1321 ttcgtcaagg ccggaactag aacccaatt ccttatgatg gaaagagaaac tgttgaggcc
1381 ttcaagggaat tcatcagtga acattcttcc tccctcaag aaaaggaatc tcgtgacgaa
30 1441 ctctaa

Figure 3B

Deduced Amino Acid Sequence of *C. parvum* Protein Disulfide Isomerase

5 MIGIRSLVSA AFLGFSCLSKVVLGGDEAHFISEHITSLTSSNFEDFIKSKEHVIVTTFAP
61 WCGHCTALEPEFKATCAEISKLSPPVHCGSVDA TENMELAQYGVSGYPTIKFFSGIDSV
121 QNYSGARSKDAFIKYIKKLTGPAVQVAESEEAIKTIFASSSAFVGRFTSKDSAEYAVFE
181 KVASGHREHNYAFIAFFQEGEQKLEVLHKDEEPVSLPMPKTVEELEAKISIMNVPLFSAI
241 SAENYSLYMSREGYTAWFCCGTNEFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQH
10 301 LLIEKFPGLVIQSVNVPSIRYMYGPAKFDSVEPLKEFMKQVSEGHHELSEKSEPIPAEQS
361 GPVTVVVGKTFEEIVFRSDKDVLLIYAQWCGHCKNLEPIYNQLGEEYKDNNDKVVIKIN
421 GPQNDIPYEGFSPRAFPTILFVKAGTRTPIPYDGKRTVEAFKEFISEHSSFPQEKESRDEL